

Introduction

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Dotplot is a tool for comparing the sequences of two genomes. **Dotplot** employs the program [Mummer](#) to generate dotplot diagrams between two genomes. It uses input DNA sequences directly for comparing genomes with similar sequences ([NUCmer](#)). It uses the six frame amino acid translation of the DNA input sequences ([PROmer](#)) for comparing genomes with dissimilar sequences (because the DNA sequence is not as highly conserved as the amino acid translation).

Dotplot

Please select 2 genomes.

Select	Ignore	Taxon Name
<input type="radio"/>	<input type="radio"/>	Bacteria
<input type="radio"/>	<input type="radio"/>	Proteobacteria
<input type="radio"/>	<input type="radio"/>	Rhizobium
<input type="radio"/>	<input checked="" type="radio"/>	Rhizobium etli 8C-3 (B)[D]
<input type="radio"/>	<input checked="" type="radio"/>	Rhizobium etli Brasil 5 (B)[D]
<input type="radio"/>	<input checked="" type="radio"/>	Rhizobium etli CFN 42 (B)[F]
<input type="radio"/>	<input checked="" type="radio"/>	Rhizobium etli CIAT 652 (B)[F]
<input type="radio"/>	<input checked="" type="radio"/>	Rhizobium etli CIAT 894 (B)[D]
<input type="radio"/>	<input checked="" type="radio"/>	Rhizobium etli GR56 (B)[D]
<input type="radio"/>	<input checked="" type="radio"/>	Rhizobium etli IE4771 (B)[D]
<input type="radio"/>	<input checked="" type="radio"/>	Rhizobium etli Kim 5 (B)[D]

Algorithm:

☒ Nucleotide sequence based comparisons
☐ Protein sequence based comparisons

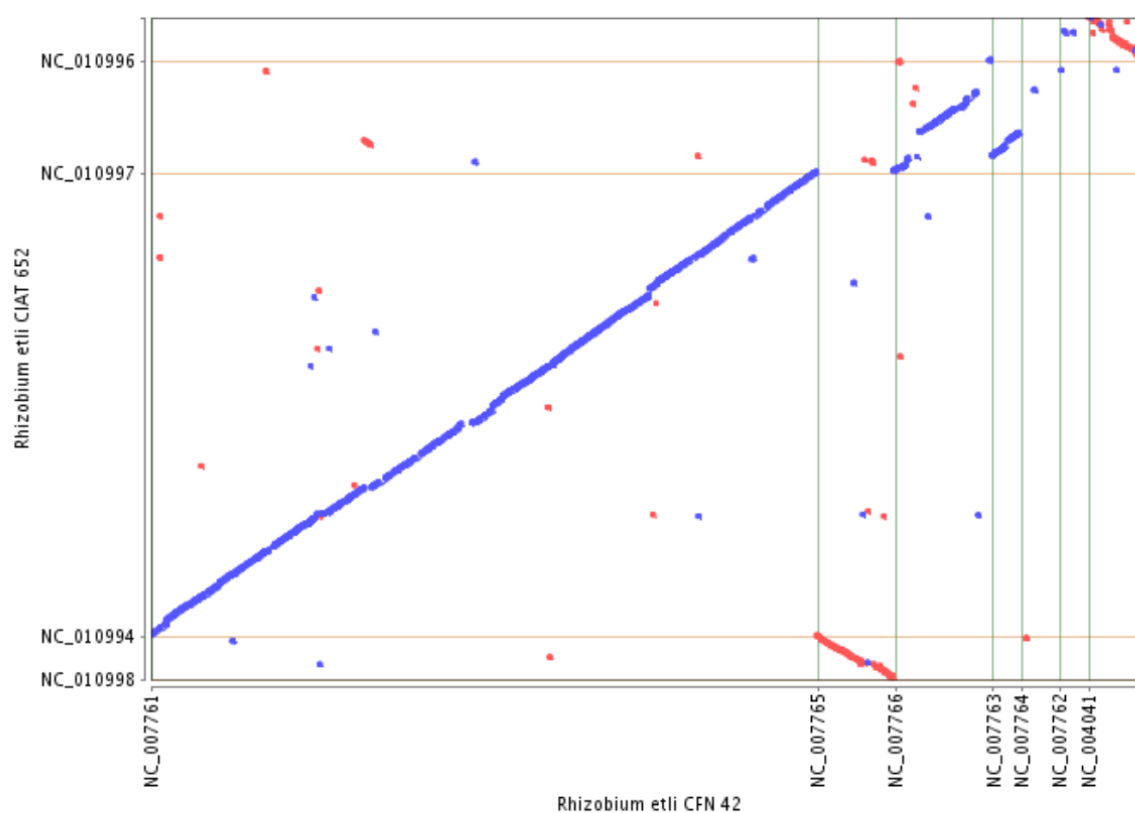
Reference:

☒ Use 1 as reference
☐ Use 2 as reference

Figure 1. Select 2 genomes for Dot Plot

Dotplot can be applied on two genomes that are selected from the list of all available or preselected genomes (Figure 1). Select which **algorithm** to use (nucleotide based comparison for genomes with similar nucleotide sequences or protein base comparison for genomes with dissimilar nucleotide sequences), and select the genome that will be used as **reference**.

Rhizobium etli CFN 42 vs. Rhizobium etli CIAT 652



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Figure 2. Dot Plot – fplot (blue), rplot (red)

The dotplot (Figure 2) consists of **blue** points for regions of similarity found on parallel strands (fplot) and **red** points for regions of similarity found on antiparallel strands (rplot). The tooltip for each point shows which plot it is and the coordinates and scaffolds of the alignment. Clicking on a point brings up the chromosomal neighborhood of the alignment of the two genomes (Figure 3). The plot can be saved either as PDF or as TIFF.

Rhizobium etli CFN 42 vs.
Rhizobium etli CIAT 652

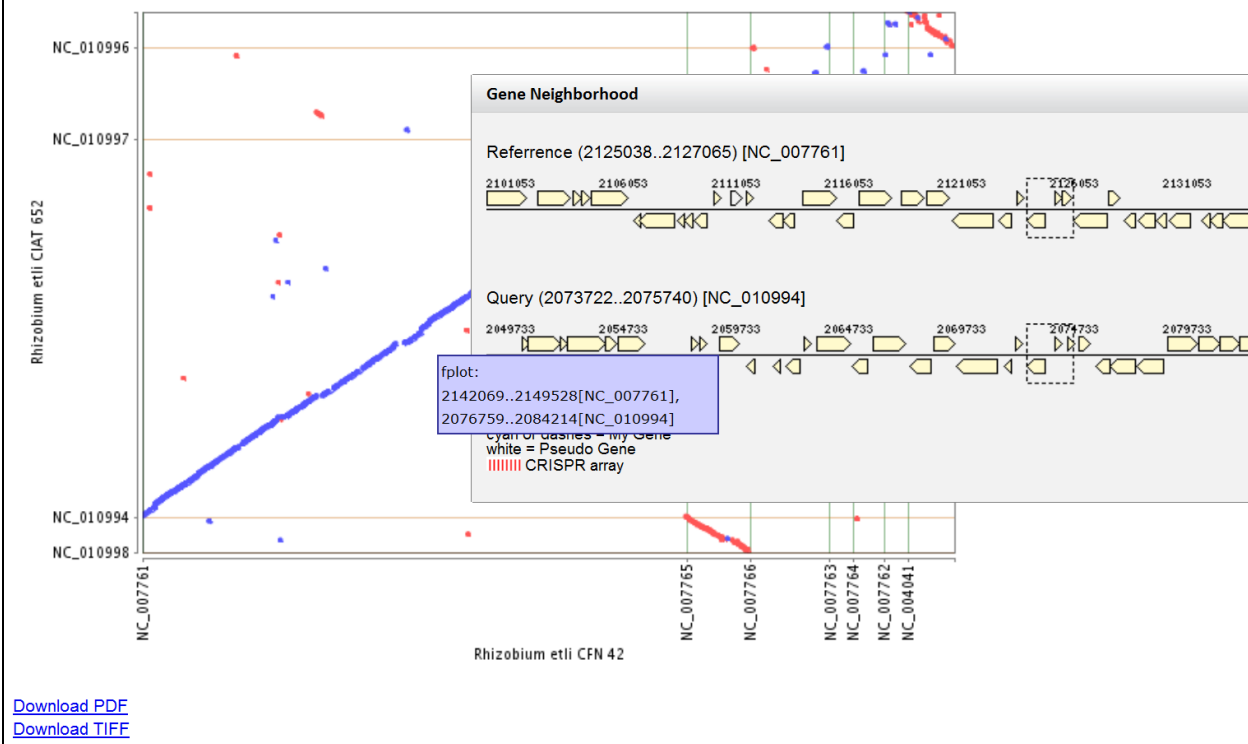


Figure 3. Dot Plot – tooltips, links to Gene Neighborhood of aligned region

Scaffold Selection IMG 3.3

When the number of scaffolds for the 2 genomes selected for Dot Plot is too high, the computation of the Dot Plot may time out. In such a scenario, the user is offered a choice to select a subset of scaffolds or to continue with the calculation using all scaffolds (Figure 5). The current cutoff is when the number of scaffold is >150 for both genomes or >300 for one of the genomes

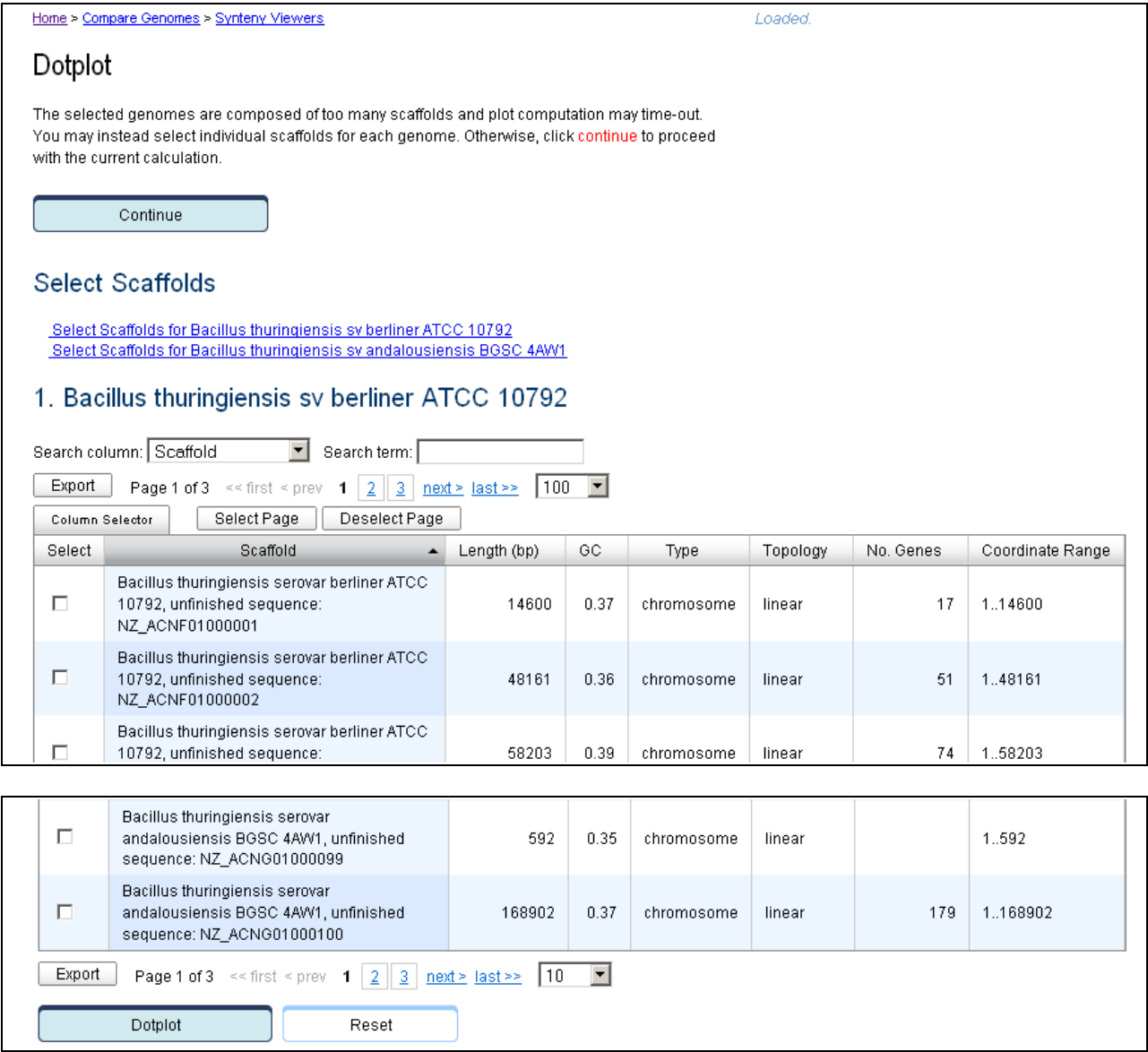


Figure 5. Select Scaffolds for Dot Plot